

09/857612

SEQUENCE LISTING

<110> E. I. du Pont de Nemours and Company
<120> Plant Lecithin:Cholesterol Acyltransferases
<130> BB1262
<140> US/09/857,612
<141> 2001-07-19
<150> 60/110,782
<151> 1998-12-03
<160> 15
<170> Microsoft Office 97
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<211> 542
<212> DNA
<213> Zea mays

<220>
<221> unsure
<222> (433)
<223> n=A, C, G, or T

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<221> unsure
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<222> (508)
<223> n=A, C, G, or T

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<222> (513)
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<220>
<221> unsure

<222> (535)

<223> n=A, C, G, or T

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 cttggcatgc tgacaatcgt cgccggcaac aatctcgcc tgccgttcgt cgaccgcgtg 180
 ggcgtcaagg gcgagtgacc gaggcctgcag agcagcctct ggccgctgccc caaccccaac 240
 gcatttagag ccggggcagcc actggtgacc acacggagca ggacgtacac ggcccacgac 300
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 gtgtgcggcc tggccatct ccgcgggtgc ccgtggcttg tgtccgtccg 420
 gggttgggct ggnacacgccc ggaanatgct ggcctaacc gggaaagacga anttcgacgt 480
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 ct 542

<210> 2

<211> 143

<212> PRT

<213> Zea mays

<400> 2

Val	Ala	His	Ser	Tyr	Gly	Gly	Thr	Leu	Ala	His	Gln	Phe	Leu	Leu	Arg
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Arg	Pro	Leu	Pro	Trp	Arg	Arg	Arg	Phe	Val	Arg	Arg	Phe	Val	Pro	Val
															30
20															
25															

Ala	Ala	Pro	Trp	Gly	Gly	Val	Val	Leu	Gly	Met	Leu	Thr	Ile	Val	Ala
35															45

Gly	Asn	Asn	Leu	Gly	Leu	Pro	Phe	Val	Asp	Pro	Leu	Ala	Leu	Lys	Gly
50															60

Glu	Tyr	Arg	Ser	Leu	Gln	Ser	Ser	Leu	Trp	Pro	Leu	Pro	Asn	Pro	Asn
65															80

Ala	Phe	Arg	Ala	Gly	Gln	Pro	Leu	Val	Thr	Thr	Arg	Ser	Arg	Thr	Tyr
85															95

Thr	Ala	His	Asp	Met	Ala	Asp	Phe	Leu	Asp	Ala	Ile	Gly	Leu	Gly	Ala
100															110

Ala	Ile	Val	Pro	Tyr	Gln	Ser	Arg	Val	Leu	Pro	Leu	Phe	Arg	Glu	Leu
115															125

Pro	Ser	Pro	Arg	Val	Pro	Val	Ala	Cys	Val	Arg	Pro	Gly	Leu	Gly	
130															140

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<211> 921

<212> DNA

<213> Zea mays

<220>

<221> unsure

<222> (884)

<223> n=A, C, G, or T

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 ctgtggaaga acagttcgga gctgctgtct cgtgactacg tgcagtgttt cgaggagcag 360
 atgagcctcg tctacgaccg tgccatcaac gaggatcgga acctcgccgg cgtcgagacg 420
 cgagtgcggca acttcggctc cacaagagcc ttcagccaca agaaccggctt caagtccagac 480
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 gtgtactccc gctacttcaa ggagctgatg gagctggtcg aggccgcgag cgagaggacc 660
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 atcgtgaatt cccgtcgccg g 921

<210> 4
 <211> 233
 <212> PRT
 <213> Zea mays

<400> 4

Met Ala Ser Ser Leu Leu Gln Gln Leu Leu Ser Leu Leu Leu Leu Leu
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Leu Pro Ser Pro Leu Arg Leu Arg Glu His Leu Ser Gly Asn His Ala
 20 25 30

Val Ser Ala Asn Asn Phe His Pro Ile Phe Leu Val Ala Gly Val Ser
 35 40 45

Cys Ser Asp Leu Glu Ala Arg Leu Thr Glu Glu Tyr Arg Pro Ser Val
 50 55 60

Pro His Cys Gly Ala Met Lys Gly Lys Gly Trp Phe Gly Leu Trp Lys
 65 70 75 80

Asn Ser Ser Glu Leu Leu Ser Arg Asp Tyr Val Gln Cys Phe Glu Glu
 85 90 95

Gln Met Ser Leu Val Tyr Asp Pro Ala Ile Asn Glu Tyr Arg Asn Leu
 100 105 110

Ala Gly Val Glu Thr Arg Val Pro Asn Phe Gly Ser Thr Arg Ala Phe
 115 120 125

Ser His Lys Asn Pro Leu Lys Ser Asp Trp Cys Leu Gly Lys Leu Arg
 130 135 140

Ala Ala Leu Glu Asp Met Gly Tyr Arg Asp Gly Asp Thr Met Phe Gly
 145 150 155 160

Ala Pro Tyr Asp Phe Arg Tyr Ala Pro Pro Ser Pro Gly Gln Thr Ser
 165 170 175

Glu Val Tyr Ser Arg Tyr Phe Lys Glu Leu Met Glu Leu Val Glu Ala
 180 185 190

Ala Ser Glu Arg Thr Arg Lys Lys Ala Val Ile Leu Gly His Ser Phe
 195 200 205

Gly Gly Met Val Ala Leu Glu Phe Val Arg Asn Thr Pro Pro Ala Trp
 210 215 220

Arg Arg Glu His Ile Glu Arg Leu Val
 225 230

<210> 5
 <211> 1217
 <212> DNA
 <213> Glycine max

<400> 5
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 ttcattacca ccaagaactc gatgattact tcaacactcc tgggggtttag acccggttcc 180
 ctcacttgg ttccaccaac tctcttctt atctcaatcc tcgtctcaag catatcaccg 240
 gatacatggc acccctggta gattcattac aaaagcttgg ctacgctgat ggtgagactc 300
 tggggggagc ccctttagac tttagatag tgcctagctgc tgaaggtcac ctttcacaag 360
 tgggttccaa gttcctcaaa gatctaaaga atttgataga agaagcaagc aattccaata 420
 atgggaagcc agtgatactt ctctccaca gtttaggagg cctatttgc ctacaactac 480
 taaaatagaaa cccccctct tggcgaaaaa aattcatcaa acacttcatt gctctttcag 540
 ctccatgggg tgggtgtata gacgaaatgt acaccttgc atctggcaac actttgggag 600
 tggccctagt ggaccctta ttagtgaggg atgaacaaag aagctccgag agtaacctt 660
 ggcttttgc taacccaaaa atttttgtc ctcaaaaaacc aatagtgata actccaattt 720
 ggccttattc agctcatgac atgggttattt ttctaaaaaga cattggtttt cctgaagggg 780
 ttatccctta tgaacacacgaa attctaccct tgatagggaa cataaaagca ccacaagtgc 840
 ctataacttgc tattatggga acgggagtgaa gaaatgtttt tatgggaaag 900
 gtgattttga tgaacggcca gaaatatcat atggggatgg tgatgaaacg gtgaacttgg 960
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 tagtaggtga gattacttca attaatttctc atgctgagct cggttaagt aatttggttt 1140
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<210> 6
 <211> 381
 <212> PRT
 <213> Glycine max

<400> 6
 Phe Ile Cys Glu Ser Trp Tyr Pro Leu Ile Lys Lys Lys Asn Gly Trp
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Phe Arg Leu Trp Phe Asp Ser Ser Val Ile Leu Ala Pro Phe Thr Gln
 20 25 30

Cys Phe Ala Glu Arg Met Thr Ile His Tyr His Gln Glu Leu Asp Asp
 35 40 45

Tyr Phe Asn Thr Pro Gly Val Glu Thr Arg Val Pro His Phe Gly Ser
 50 55 60

Thr Asn Ser Leu Leu Tyr Leu Asn Pro Arg Leu Lys His Ile Thr Gly
 65 70 75 80

Tyr Met Ala Pro Leu Val Asp Ser Leu Gln Lys Leu Gly Tyr Ala Asp
 85 90 95

Gly Glu Thr Leu Phe Gly Ala Pro Tyr Asp Phe Arg Tyr Gly Leu Ala

100	105	110
Ala Glu Gly His Pro Ser Gln Val Gly Ser Lys Phe Leu Lys Asp Leu		
115	120	125
Lys Asn Leu Ile Glu Glu Ala Ser Asn Ser Asn Asn Gly Lys Pro Val		
130	135	140
Ile Leu Leu Ser His Ser Leu Gly Gly Leu Phe Val Leu Gln Leu Leu		
145	150	155
Asn Arg Asn Pro Pro Ser Trp Arg Lys Lys Phe Ile Lys His Phe Ile		
165	170	175
Ala Leu Ser Ala Pro Trp Gly Gly Ala Ile Asp Glu Met Tyr Thr Phe		
180	185	190
Ala Ser Gly Asn Thr Leu Gly Val Pro Leu Val Asp Pro Leu Leu Val		
195	200	205
Arg Asp Glu Gln Arg Ser Ser Glu Ser Asn Leu Trp Leu Leu Pro Asn		
210	215	220
Pro Lys Ile Phe Gly Pro Gln Lys Pro Ile Val Ile Thr Pro Ile Arg		
225	230	235
Pro Tyr Ser Ala His Asp Met Val Asp Phe Leu Lys Asp Ile Gly Phe		
245	250	255
Pro Glu Gly Val Tyr Pro Tyr Glu Thr Arg Ile Leu Pro Leu Ile Gly		
260	265	270
Asn Ile Lys Ala Pro Gln Val Pro Ile Thr Cys Ile Met Gly Thr Gly		
275	280	285
Val Gly Thr Leu Glu Thr Leu Phe Tyr Gly Lys Gly Asp Phe Asp Glu		
290	295	300
Arg Pro Glu Ile Ser Tyr Gly Asp Gly Asp Gly Thr Val Asn Leu Val		
305	310	315
Ser Leu Leu Ala Leu Gln Ser Leu Trp Lys Glu Glu Lys Asn Gln Tyr		
325	330	335
Leu Lys Val Val Lys Ile Asp Gly Val Ser His Thr Ser Ile Leu Lys		
340	345	350
Asp Glu Val Ala Leu Asn Glu Ile Val Gly Glu Ile Thr Ser Ile Asn		
355	360	365
Ser His Ala Glu Leu Gly Leu Ser Asn Leu Phe Ser Gly		
370	375	380
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<211> 1440		
<212> DNA		
<213> Zea mays		
<400> 7		
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cggcgcgagg	tccctctcca	cccgctgggt	ctgggtcccc	ggctgacgtg	cagcgagctg	180
gacgcgcgac	tcacggacgc	ctaccgcccc	ttcccgcccg	cgtgcgtatga	aggggaaggg	240
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atggagcaga	tggccctcg	ctacgacccc	gtcgcaacg	actaccggaa	cctggcccg	360
gtcgagacgc	gcgtgcgc	tttcggctcc	tcccgggat	tccagaagaa	cccgagacac	420
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gacggcgaca	cctgttccg	ggccccgtac	gacccctccgt	acgccccggc	gtgccccggc	540
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gagcagctcg	tctactgg	cggcgacttc	gacgcgaccc	cggagatagt	gtacggcgc	1140
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ccggaacaga	acaagggtgt	caagtcgatc	aaagattcgt	gggcccagca	cggtactatt	1260
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<210> 8
<211> 434
<212> PRT
<213> Zea mays

<400> 8

Met Ala Arg Ile Pro Gln Val Leu Ala Pro Leu Leu Leu Leu Leu Leu Leu
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Pro Ala Gly Leu Arg Glu Leu Met Ile Asp Arg Arg Pro Leu Pro Lys
20 25 30

Arg Cys Arg Arg Glu Val Leu Leu His Pro Leu Val Leu Val Pro Gly
35 40 45

Leu Thr Cys Ser Glu Leu Asp Ala Arg Leu Thr Asp Ala Tyr Arg Pro
50 55 60

Phe Arg Ala Ala Cys Asp Glu Gly Glu Gly Leu Val Arg Leu Trp Thr
 65 70 75 80

Asp Cys Ser Asp Lys Pro Ala His His Tyr Val Ser

85 90 95
Gln Met Ala Ile Val Thr Leu Pro Val Asp

100 105 110

115 120 125

130 135 140

145 150 155 160

Gly Ala Pro Tyr Asp Leu Arg Tyr Ala Pro Pro Val Pro Gly Gln Pro
 165 170 175
 Ser Arg Ser Ser Pro Ala Thr Ser Val Gly Trp Pro Ser Leu Val Glu
 180 185 190
 Asp Ala Ser Arg Lys Asn Arg Gly Arg Lys Val Ile Leu Phe Gly His
 195 200 205
 Ser Phe Gly Gly Met Val Ala Leu Glu Phe Val Arg Ser Thr Pro Met
 210 215 220
 Ala Trp Arg Asp Arg Tyr Ile Lys His Leu Phe Leu Val Ala Pro Val
 225 230 235 240
 Pro Ala Glu Gly Phe Val Lys Pro Leu Gln Tyr Phe Val Ser Gly Ser
 245 250 255
 Asn Leu Met Tyr Val Pro Thr Val Ser Ser Leu Glu Pro Ala Phe Arg
 260 265 270
 Pro Met Trp Arg Thr Phe Glu Ser Ser Leu Val Asn Phe Pro Ser Pro
 275 280 285
 Ala Val Phe Gly Arg Arg Pro Leu Val Val Thr Ala Arg Arg Asn Tyr
 290 295 300
 Ser Ala Tyr Asp Leu Glu Asp Leu Leu Val Ala Val Gly Tyr Gly Ala
 305 310 315 320
 Gly Val Glu Pro Phe Arg Arg Ala Val Pro Lys Met Ser Tyr Phe
 325 330 335
 Gln Ala Pro Met Val Pro Thr Thr Cys Met Asn Gly Val Gly Asn Asp
 340 345 350
 Thr Pro Glu Gln Leu Val Tyr Trp Asp Gly Asp Phe Asp Ala Thr Pro
 355 360 365
 Glu Ile Val Tyr Gly Asp Gly Asp Asn Ser Ile Asn Leu Val Ser Met
 370 375 380
 Leu Ala Phe Asp Glu Lys Met Arg Arg Gln Pro Glu Gln Asn Lys Val
 385 390 395 400
 Tyr Lys Ser Ile Lys Ile Arg Gly Ala Gln His Gly Thr Ile Val Thr
 405 410 415
 Asp Asp Thr Ala Leu Lys Arg Val Met His Glu Ile Leu Glu Ala Asn
 420 425 430

Arg Ser

<210> 9
 <211> 1500
 <212> DNA
 <213> Zea mays

<220>

<221> unsure
<222> (536)
<223> n=A, C, G, or T

<400> 9

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tgggtgggt	gcccggtac	gccaccaacg	agctcgacgc	gcccctcagc	gagctgtacc	180
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acgtgacgccc	gatgatggtc	atgggagacg	gcccacgggt	ggtcaacactg	gtgagctcc	1140
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tcacgaaaag	tttagataac	aaattttcat	cgttagcatg	taagggaaata	ggtggtaagc	1380
tctaaatttt	acattattag	ttccgattaa	gggctaaaca	tgaggatgt	acctcctgtat	1440
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<210> 10
<211> 417
<212> PRT
<213> Zea mays

<400> 10

Met Val His Asp Met Ala Ser Cys Ser Arg Gly Gly Thr Ile Val Leu
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Ser Lys Phe Ala Ser Thr Thr Arg Arg Ala Pro Lys Gln Leu Pro Pro
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Val Val Val Val Pro Gly Tyr Ala Thr Asn Glu Leu Asp Ala Arg Leu
35 40 45

Thr Glu Leu Tyr His Pro Ser Ser Pro Arg Cys Ala His Lys Gly Lys
 50 55 60

Gly Trp Phe Arg Leu Tyr Leu Asn Tyr Thr Ala Leu Glu Asp Ala Ala
 65 70 75 80

Asp Val Arg Cys Phe Ala Glu Gln Met Ala Thr Ala Tyr Asp Ala Ala
85 90 95

Ser Asp Asp Tyr Arg Asn Ala Gln Gly Val Glu Thr Arg Val Pro Phe
 100 105 110

Phe Gly Ser Thr Arg Ala Phe Arg Tyr Pro Asp Pro Asp Arg Arg Asn
115 120 125

Phe Ser Tyr Met Asp Lys Phe Val Ser Arg Leu Glu Arg Leu Ala Tyr
 130 135 140
 Arg Asp Gly Glu Asn Leu Phe Gly Ala Pro Tyr Asp Phe Arg Tyr Ala
 145 150 155 160
 Val Ala Pro Pro Gly His Pro Ser Arg Val Ala Asp Ala Phe Phe Gly
 165 170 175
 Arg Leu Arg Arg Leu Val Glu Arg Ala Ser Arg Ala Asn Gly Gly Gly
 180 185 190
 Pro Val Thr Ile Val Ala His Ser Tyr Gly Gly Thr Val Ala His Gln
 195 200 205
 Phe Leu Leu Arg Arg Pro Leu Pro Trp Arg Arg Arg Phe Val Arg Arg
 210 215 220
 Phe Val Pro Val Ala Ala Pro Trp Gly Gly Val Val Leu Gly Met Leu
 225 230 235 240
 Thr Ile Val Ala Gly Asn Asn Leu Gly Leu Pro Phe Val Asp Pro Leu
 245 250 255
 Ala Leu Lys Gly Glu Tyr Arg Ser Leu Gln Ser Ser Leu Trp Pro Leu
 260 265 270
 Pro Asn Pro Asn Ala Phe Arg Ala Gly Gln Pro Leu Val Thr Thr Arg
 275 280 285
 Ser Arg Thr Tyr Thr Ala His Asp Met Ala Asp Phe Leu Asp Ala Ile
 290 295 300
 Gly Leu Gly Ala Ala Ile Val Pro Tyr Gln Ser Arg Val Leu Pro Leu
 305 310 315 320
 Phe Arg Glu Leu Pro Ser Pro Arg Val Pro Val Ala Cys Val Val Gly
 325 330 335
 Val Gly Leu Asp Thr Pro Glu Met Leu Ala Tyr Pro Gly Asp Asp Phe
 340 345 350
 Asp Val Thr Pro Met Met Val Met Gly Asp Gly Asp Gly Leu Val Asn
 355 360 365
 Leu Val Ser Leu Leu Ala Val Asp Pro Ala Trp Arg Leu Pro Thr Ala
 370 375 380
 Tyr Phe Arg Met Leu Lys Val Arg Asn Val Ser His Thr Gly Leu Phe
 385 390 395 400
 Val Asp Asp Ala Ala Leu Ala Val Ile Ile Ser Ala Ile Leu Arg Pro
 405 410 415

Asn

<210> 11
 <211> 1660

<212> DNA

<213> Zea mays

<400> 11

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 agacaccatg ttcggagccc cctacgactt ccgctacgcg ccggccgtccc ccggccagac 600
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 gttatgggtt aacgtcaatt gcttgctca tgaacttgct gtgataagga aagaccacaa 1560
 ttatgggttggg cttgtcgtgt gcgttgacc gtataatgtt aataaaaaca agagtaaaat 1620
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<210> 12

<211> 439

<212> PRT

<213> Zea mays

<400> 12

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Leu Pro Ser Pro Leu Arg Leu Arg Glu His Leu Ser Gly Asn His Ala
 20 25 30

Val Ser Ala Asn Asn Phe His Pro Ile Phe Leu Val Ala Gly Val Ser
 35 40 45

Cys Ser Asp Leu Glu Ala Arg Leu Thr Glu Glu Tyr Arg Pro Ser Val
 50 55 60

Pro His Cys Gly Ala Met Lys Gly Lys Gly Trp Phe Gly Leu Trp Lys
 65 70 75 80

Asn Ser Ser Glu Leu Leu Ser Arg Asp Tyr Val Gln Cys Phe Glu Glu
 85 90 95

Gln Met Ser Leu Val Tyr Asp Pro Ala Ile Asn Glu Tyr Arg Asn Leu
 100 105 110

Ala Gly Val Glu Thr Arg Val Pro Asn Phe Gly Ser Thr Arg Ala Phe
 115 120 125
 Ser His Lys Asn Pro Leu Lys Ser Asp Trp Cys Leu Gly Lys Leu Arg
 130 135 140
 Ala Ala Leu Glu Asp Met Gly Tyr Arg Asp Gly Asp Thr Met Phe Gly
 145 150 155 160
 Ala Pro Tyr Asp Phe Arg Tyr Ala Pro Pro Ser Pro Gly Gln Thr Ser
 165 170 175
 Glu Val Tyr Ser Arg Tyr Phe Lys Glu Leu Met Glu Leu Val Glu Ala
 180 185 190
 Ala Ser Glu Arg Thr Arg Lys Lys Ala Val Ile Leu Gly His Ser Phe
 195 200 205
 Gly Gly Met Val Ala Leu Glu Phe Val Arg Asn Thr Pro Pro Ala Trp
 210 215 220
 Arg Arg Glu His Ile Glu Arg Leu Val Leu Val Ala Pro Thr Leu Pro
 225 230 235 240
 Gly Gly Phe Leu Glu Pro Val Arg Asn Phe Ala Ser Gly Thr Asp Ile
 245 250 255
 Leu Tyr Val Pro Ala Thr Thr Pro Leu Ala Thr Arg Ala Met Trp Arg
 260 265 270
 Ser Phe Glu Ser Ala Ile Val Asn Phe Pro Ser Pro Ala Val Phe Gly
 275 280 285
 Arg Leu Gln Ala Pro Leu Val Val Thr Arg Glu Arg Asn Tyr Ser Ala
 290 295 300
 Ser Ala His Asp Met Glu Arg Phe Leu Ala Ala Val Gly Ser Gly Glu
 305 310 315 320
 Ala Ala Glu Pro Phe Arg Arg Arg Ala Val Pro Lys Met Gly Ser Phe
 325 330 335
 Ala Ala Pro Met Val Pro Met Thr Tyr Ile Ser Gly Val Gly Asn Arg
 340 345 350
 Thr Pro Leu Arg Leu Val Phe Trp Gly Glu Asp Phe Asp Ala Ala Pro
 355 360 365
 Glu Val Ala Ala Tyr Gly Asp Arg Asp Gly Lys Ile Asn Leu Ile Ser
 370 375 380
 Val Leu Ala Phe Glu Lys Glu Met Arg Arg Gln Pro Glu Gln Lys Lys
 385 390 395 400
 Gln Phe Lys Ser Ile Lys Ile Asn Lys Ala Gln His Ser Thr Ile Val
 405 410 415
 Thr Asp Asp Phe Ala Leu His Arg Val Ile Gln Glu Ile Val Glu Ala
 420 425 430

Asn Asn Gln Lys Ile Pro Ser
435

<210> 13

<211> 1332

<212> DNA

<213> Glycine max

<400> 13

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ctaataccag gtaacggagg gaaccaacta gaagcaaggt tgaccaatca gtacaagccc 180
tctactttca tctgcgaatc atggtaccct ctcataaaga aaaagaatgg atggttcaga 240
ctttggttt attccagtgt catactgtct cctttcactt aatgcgttgc cgaacgcatt 300
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gtccctcaact ttggttccac caactctt ctctatctca atcctcgctt caagcatatc 420
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<210> 14

<211> 443

<212> PRT

<213> Glycine max

<400> 14

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Thr Val Thr Val Val Val Met Leu Ser Leu Leu Cys Thr Cys Gly
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Ala Ser Asn Leu Asp Pro Leu Ile Leu Ile Pro Gly Asn Gly Gly Asn
35 40 45

Gln Leu Glu Ala Arg Leu Thr Asn Gln Tyr Lys Pro Ser Thr Phe Ile
50 55 60

Cys Glu Ser Trp Tyr Pro Leu Ile Lys Lys Lys Asn Gly Trp Phe Arg
65 70 75 80

Leu Trp Phe Asp Ser Ser Val Ile Leu Ala Pro Phe Thr Gln Cys Phe
85 90 95

Ala Glu Arg Met Thr Leu His Tyr His Gln Glu Leu Asp Asp Tyr Phe
100 105 110

Asn Thr Pro Gly Val Glu Thr Arg Val Pro His Phe Gly Ser Thr Asn
 115 120 125
 Ser Leu Leu Tyr Leu Asn Pro Arg Leu Lys His Ile Thr Gly Tyr Met
 130 135 140
 Ala Pro Leu Val Asp Ser Leu Gln Lys Leu Gly Tyr Ala Asp Gly Glu
 145 150 155 160
 Thr Leu Phe Gly Ala Pro Tyr Asp Phe Arg Tyr Gly Leu Ala Ala Glu
 165 170 175
 Gly His Pro Ser Gln Val Gly Ser Lys Phe Leu Lys Asp Leu Lys Asn
 180 185 190
 Leu Ile Glu Glu Ala Ser Asn Ser Asn Asn Gly Lys Pro Val Ile Leu
 195 200 205
 Leu Ser His Ser Leu Gly Gly Leu Phe Val Leu Gln Leu Leu Asn Arg
 210 215 220
 Asn Pro Pro Ser Trp Arg Lys Lys Phe Ile Lys His Phe Ile Ala Leu
 225 230 235 240
 Ser Ala Pro Trp Gly Gly Ala Ile Asp Glu Met Tyr Thr Phe Ala Ser
 245 250 255
 Gly Asn Thr Leu Gly Val Pro Leu Val Asp Pro Leu Leu Val Arg Asp
 260 265 270
 Glu Gln Arg Ser Ser Glu Ser Asn Leu Trp Leu Leu Pro Asn Pro Lys
 275 280 285
 Ile Phe Gly Pro Gln Lys Pro Ile Val Ile Thr Pro Ile Arg Pro Tyr
 290 295 300
 Ser Ala His Asp Met Val Asp Phe Leu Lys Asp Ile Gly Phe Pro Glu
 305 310 315 320
 Gly Val Tyr Pro Tyr Glu Thr Arg Ile Leu Pro Leu Ile Gly Asn Ile
 325 330 335
 Lys Ala Pro Gln Val Pro Ile Thr Cys Ile Met Gly Thr Gly Val Gly
 340 345 350
 Thr Leu Glu Thr Leu Phe Tyr Gly Lys Gly Asp Phe Asp Glu Arg Pro
 355 360 365
 Glu Ile Ser Tyr Gly Asp Gly Asp Gly Thr Val Asn Leu Val Ser Leu
 370 375 380
 Leu Ala Leu Gln Ser Leu Trp Lys Glu Glu Lys Asn Gln Tyr Leu Lys
 385 390 395 400
 Val Val Lys Ile Asp Gly Val Ser His Thr Ser Ile Leu Lys Asp Glu
 405 410 415
 Val Ala Leu Asn Glu Ile Val Gly Glu Ile Thr Ser Ile Asn Ser His
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Ala Glu Leu Gly Leu Ser Asn Leu Phe Ser Gly
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<210> 15
<211> 432
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<400> 15
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1 5 10 15

Val Val Thr Met Thr Ser Met Cys Gln Ala Val Gly Ser Asn Val Tyr
20 25 30

Pro Leu Ile Leu Val Pro Gly Asn Gly Gly Asn Gln Leu Glu Val Arg
35 40 45

Leu Asp Arg Glu Tyr Lys Pro Ser Ser Val Trp Cys Ser Ser Trp Leu
50 55 60

Tyr Pro Ile His Lys Lys Ser Gly Gly Trp Phe Arg Leu Trp Phe Asp
65 70 75 80

Ala Ala Val Leu Leu Ser Pro Phe Thr Arg Cys Phe Ser Asp Arg Met
85 90 95

Met Leu Tyr Tyr Asp Pro Asp Leu Asp Asp Tyr Gln Asn Ala Pro Gly
100 105 110

Val Gln Thr Arg Val Pro His Phe Gly Ser Thr Lys Ser Leu Leu Tyr
115 120 125

Leu Asp Pro Arg Leu Arg Asp Ala Thr Ser Tyr Met Glu His Leu Val
130 135 140

Lys Ala Leu Glu Lys Lys Cys Gly Tyr Val Asn Asp Gln Thr Ile Leu
145 150 155 160

Gly Ala Pro Tyr Asp Phe Arg Tyr Gly Leu Ala Ala Ser Gly His Pro
165 170 175

Ser Arg Val Ala Ser Gln Phe Leu Gln Asp Leu Lys Gln Leu Val Glu
180 185 190

Lys Thr Ser Ser Glu Asn Glu Gly Lys Pro Val Ile Leu Leu Ser His
195 200 205

Ser Leu Gly Gly Leu Phe Val Leu His Phe Leu Asn Arg Thr Thr Pro
210 215 220

Ser Trp Arg Arg Lys Tyr Ile Lys His Phe Val Ala Leu Ala Ala Pro
225 230 235 240

Trp Gly Gly Thr Ile Ser Gln Met Lys Thr Phe Ala Ser Gly Asn Thr
245 250 255

Leu Gly Val Pro Leu Val Asn Pro Leu Leu Val Arg Arg His Gln Arg
260 265 270

Thr Ser Glu Ser Asn Gln Trp Leu Leu Pro Ser Thr Lys Val Phe His
275 280 285

Asp Arg Thr Lys Pro Leu Val Val Thr Pro Gln Val Asn Tyr Thr Ala
290 295 300

Tyr Glu Met Asp Arg Phe Phe Ala Asp Ile Gly Phe Ser Gln Gly Val
305 310 315 320

Val Pro Tyr Lys Thr Arg Val Leu Pro Leu Thr Glu Glu Leu Met Thr
325 330 335

Pro Gly Val Pro Val Thr Cys Ile Tyr Gly Arg Gly Val Asp Thr Pro
340 345 350

Glu Val Leu Met Tyr Gly Lys Gly Gly Phe Asp Lys Gln Pro Glu Ile
355 360 365

Lys Tyr Gly Asp Gly Asp Gly Thr Val Asn Leu Ala Ser Leu Ala Ala
370 375 380

Leu Lys Val Asp Ser Leu Asn Thr Val Glu Ile Asp Gly Val Ser His
385 390 395 400

Thr Ser Ile Leu Lys Asp Glu Ile Ala Leu Lys Glu Ile Met Lys Gln
405 410 415

Ile Ser Ile Ile Asn Tyr Glu Leu Ala Asn Val Asn Ala Val Asn Glu
420 425 430